

**Supplemental Table 3: Means of Smith-Waterman scores.**

Experiment	Control mean	Experimental mean	t	p-value
35S::amiR-lfy-1( <i>MIR172a</i> )	48.3	47.0 (47.0)	4.727 (4.358)	0.9999 (0.9999)
35S::amiR-mads-1( <i>MIR172a</i> )	52.2	52.4 (53.1)	-0.571 (-1.693)	0.3036 (0.9530)
35S::amiR-mads-2( <i>MIR319a</i> )	54.1	52.3 (52.6)	4.428 (7.283)	0.9999 (1.0000)

All genes present in the control (wild-type Col-0) were compared with the genes significantly downregulated in response to amiRNA overexpression (experiment). One-sided student's t-tests suggest that the means of the experimental samples are not significantly higher than those of the controls. (In most cases, they are actually lower.) Significant expression changes were corrected for multiple testing at 1% FDR (Benjamini, Y., and Yekutieli, D. (2001). The control of the false discovery rate in multiple testing under dependency. *Ann. Statist.* 29, 1165-1188), with a common change of 1.5 fold relative to the wild-type control. As additional information, genes significantly changed under the logit-T algorithm ( $p < 0.025$ ) are shown in parentheses.